

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/758,003

DATE: 07/30/2001

TIME: 12:09:42

Input Set: N:\CrF3\RULE60\09758003.txt

Output Set: N:\CRF3\07302001\I758003.raw

52	ATG	CAA	CCA	GAT	ATG	TCC	TTG	AAT	GTC	ATT	AAG	ATG	AAA	TCC	AAT	GAC	43
53	Met	Gln	Pro	Asp	Met	Ile	Leu	Asn	Val	Ile	Lys	Met	Lys	Ser	Ile	Asp	
54	1				5					10					15		
55	TTC	CTG	GAG	AGT	KA	CAA	CTG	GAC	AGC	GAA	GCG	TTT	GCG	AAG	GTC	TCT	56
56	Phe	Leu	Glu	Ser	Ala	Glu	Leu	Asp	Ser	Ile	Gly	Ile	Gly	Lys	Val	Ser	
57					20					25					30		
58	CTG	TGT	TTC	CAI	AGA	AAC	CAG	GGA	CTG	ATG	ATG	ATG	AAA	AAT	GTC	TAC	144
59	Leu	Cys	Phe	His	Arg	Thr	Gln	Gly	Leu	Met	Ile	Met	Lys	Thr	Val	Tyr	
60					35					40					45		
61	AAG	GGG	CCC	AAI	TCT	ATT	GAG	CAI	AAI	GAG	CCC	TTC	TTG	TAG	GAG	GCG	149
62	Lys	Gly	Pro	Asn	Cys	Ile	Glu	His	Asn	Glu	Ala	Ile	Leu	Ile	Glu	Asn	
63					50					55					60		
64	AAG	ATG	ATG	AAC	AGA	CTG	AGA	CAI	AGC	GGG	GTC	GTC	GTC	AAG	TTC	CTG	240
65	Lys	Met	Met	Asn	Arg	Leu	Arg	His	Ser	Arg	Val	Val	Lys	Leu	Ile	Gly	
66					65					70					75		
67	GTC	ATC	ATA	GAG	AAI	GGG	AAG	TAC	TCC	CTG	GTC	ATG	GAG	TAC	ATG	GAG	285
68	Val	Ile	Ile	Glu	Ala	Gly	Lys	Tyr	Ser	Leu	Val	Met	Glu	Tyr	Met	Glu	
69					75					80					85		
70	AAG	GGC	AAI	CTG	ATG	CAC	GTG	CTG	AAI	GCC	GAG	ATG	AGT	ACT	CCG	CTT	330
71	Lys	Gly	Asn	Leu	Met	His	Val	Ile	Lys	Ala	Glu	Met	Ser	Thr	Pro	Leu	
72					100					105					110		
73	TCT	GTA	AAA	GGA	AGG	ATA	ATT	TTG	GAA	ATC	ATT	GAA	GGA	ATG	TGC	TAC	384
74	Ser	Val	Lys	Gly	Arg	Ile	Ile	Leu	Glu	Ile	Ile	Gly	Met	Cys	Tyr		
75					115					120					125		
76	TTA	CAT	GGA	AAA	GGC	GTG	ATA	CAC	AAG	GAC	CTG	AAG	CCT	GAA	AAT	ATC	433
77	Leu	His	Gly	Lys	Gly	Val	Ile	His	Lys	Asp	Leu	Lys	Pro	Ile	Asn	Ile	
78					130					135					140		
79	CTT	GTT	GAT	AAT	GAC	TTC	CAC	ATT	AAG	ATC	GCA	GAC	CTC	GGC	CTT	GCC	480
80	Leu	Val	Asp	Asn	Asp	Phe	His	Ile	Lys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	
81					145					150					155		
82	TCC	TTT	AAG	ATG	TGG	AGC	AAA	CTG	AAT	AAT	GAA	GAG	CAC	AAT	GAG	CTG	528
83	Ser	Phe	Lys	Met	Trp	Ser	Lys	Leu	Asn	Asn	Glu	Gly	His	Asn	Glu	Leu	
84					155					160					175		
85	AGG	GAA	GTG	GAC	GGC	ACC	GCT	AAG	AAG	AAT	GGC	GGC	ACC	CTC	TAC	TAC	576
86	Arg	Glu	Val	Asp	Gly	Thr	Ala	Lys	Lys	Asn	Gly	Gly	Thr	Leu	Tyr	Tyr	
87					160					165					190		
88	ATG	GCG	CCC	GAG	CTG	AAT	GAC	GTC	AAC	GCA	AAG	CCC	ACA	GAG	ATG	ATG	624
89	Met	Ala	Pro	Glu	His	Ile	Asn	Asp	Val	Asn	Ala	Lys	Pro	Thr	Glu	Lys	
90					190					200					205		
91	TCG	GAT	GTG	TAC	AGC	TTT	GCT	GTA	GTA	CTC	TGG	GGG	ATA	TTT	GCA	AAT	673
92	Ser	Asp	Val	Tyr	Ser	Phe	Ala	Val	Val	Leu	Trp	Ala	Ile	Phe	Ala	Asn	
93					210					215					220		
94	AAG	GAG	CCA	TAT	AAA	AAT	GCT	ATC	TGT	GAG	CAG	CAG	TAS	TTG	ATA	ATG	720
95	Lys	Glu	Pro	Tyr	Glu	Asn	Ala	Ile	Cys	Glu	Gln	Gln	Leu	Ile	Met	Cys	
96					225					230					235		
97	ATA	AAA	TCT	GGG	AAI	AGG	CCA	GAT	GTG	GAT	SAC	ATC	ACT	GA3	TAC	TGG	763
98	Ile	Lys	Ser	Gly	Asn	Arg	Pro	Asp	Val	Asp	Asp	Ile	Thr	Glu	Tyr	Cys	
99					240					250					255		
100	CCA	AGA	GAA	ATT	ATC	AGT	CTC	ATG	AAG	CTC	TGC	TGG	GAA	GGG	AAT	CCG	816

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101	Pro	Arg	Glu	Ile	Ile	Ser	Leu	Met	Lys	Leu	lys	Trp	Glu	Ala	Asn	Pro
102																
	261															370
103	GAA	GCT	CGG	CCT	ACA	TTT	TCT	GCT	ATP	GAA	GAA	AAA	TTT	AGG	CCT	TTT
104	Glu	Gln	Gly	Gln	Arg	Tyr	Ser	Arg	Pro	Gly	Ile	Glu	Lys	Pro	Arg	Pro
105																
	275															294
106	TAT	TTA	ATP	CAA	TTA	GAA	AAA	AGT	GTA	GAA	GAG	GAA	GTC	AGG	AGT	TTA
107	Tyr	Leu	Ser	Glu	Leu	Glu	Ser	Val	Glu	Glu	Arg	Val	lys	Ser	Leu	
108																
	290															309
109	AAG	AAA	GAG	TAT	TTA	ATC	GAA	ATP	GCA	CTT	GTC	AAG	AGA	ATC	GAC	TTT
110	Lys	Lys	Glu	Gln	Tyr	Ser	Arg	Gln	Glu	Ala	Val	Val	Lys	Arg	Met	Gln
111																
	305															324
112	CTT	CAA	CPT	GAT	TGT	CTG	GCA	CTA	CCT	TCA	AGC	GCG	TCA	ATC	TCA	GTC
113	Leu	Gln	Leu	Asn	Cys	Val	Ala	Val	Pro	Ser	Ser	Arg	Ser	Asn	Ser	Ala
114																
	325															334
115	ACA	GAA	CAG	CCT	GCT	TTA	CTG	CAC	AGT	TCC	CAG	GGA	CTT	GGG	ATG	GGT
116	Thr	Glu	Gln	Pro	Gly	Ser	Leu	His	Ser	Ser	Gln	Gly	Leu	Met	Gly	
117																
	340															359
118	CCT	GTG	GAG	GAG	TCA	GGG	TTT	GCT	CCT	TCC	CTG	GAG	CAC	GCA	CAA	GAA
119	Pro	Val	Glu	Glu	Ser	Trp	Phe	Ala	Pro	Ser	Leu	Glu	His	Pro	Gln	Glu
120																
	355															364
121	GAG	AAT	GAG	CCC	ATG	CGG	AGT	AAA	CTC	CAA	GAC	GAA	GCC	AAC	TAC	
122	Glu	Asn	Glu	Glu	Pro	Ser	Ser	Leu	Ser	Gln	Asp	Glu	Ala	Asn	Tyr	
123																
	370															389
124	CAT	CTT	TAT	GCG	AGC	ATG	GAC	AGG	CAG	ACG	AGC	CAG	CCC	AGA		
125	His	Leu	Tyr	Gly	Ser	Arg	Met	Asp	Arg	Gln	Thr	Lys	Gln	Gln	Pro	Arg
126																
	385															404
127	CAG	AAT	GTG	GCT	TAC	AAC	AGA	GAG	GAA	AGG	AGA	GCG	AGG	GTC	TCC	
128	Gln	Asn	Val	Ala	Tyr	Asn	Arg	Glu	Glu	Glu	Glu	Arg	Arg	Arg	Val	Ser
129																
	405															414
130	CAT	GAC	CCT	TTT	GCA	CAG	CAA	AGA	CCT	TAC	GAG					

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150	515	520	525	
151	ATA AAA TAT ACC ATA TAC AAT AGT ACT GAG ATT CAG ATT GGA GCC TAC			1632
152	Ile Lys Tyr Thr Ile Tyr Asn Ser Thr Asp Ile Gln Ile Gly Ala Tyr			
153	530	535	540	
154	ATC TAT ATG GAG ATT GAT GGG AGG AGT TAA TCA CTA CTA GAT AGC ACA			1680
155	Asn Tyr Met Glu Ile Gly Gly Thr Ser Ser Ser Leu Leu Asp Ser Thr			
156	545	550	555	560
157	ATC ATG AAC TTC AAA GAA GAG CCA CCT GCT AAC TAC CAA GAT ATC TTT			1728
158	Asn Thr Asn Ile Lys Glu Glu Pro Ala Ala Lys Tyr Glu Ala Ile Pro			
159	565	570	575	
160	GAT AAC ACC ACT AGT CTG AGC GAT AAA CAT CTG GAC CCA ATC AGG GAA			1776
161	Asp Asn Thr Thr Ser Leu Thr Asp Lys His Leu Asp Pro Ile Arg Glu			
162	580	585	590	
163	ATC CTG GGA AAG AAC TGG AAA AAC TGT GAT CCG CGT AAA CGG GGC TTC ACA			1824
164	Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys Leu Gly Phe Thr			
165	595	600	605	
166	CAG TCT CAG ATT GAT GAA ATT GAT GAT TAT GAG CGA GAT GGA CTG			1872
167	Gln Ser Gln Ile Asp Glu Ile Asp His Asp Tyr Glu Arg Asp Gly Leu			
168	610	615	620	
169	AAA GAA AAG GTT TAC CAG ATG CTC CAA AAG TGG GTG ATG AGG GAA GGC			1920
170	Lys Glu Lys Val Tyr Glu Met Leu Gln Lys Trp Val Met Arg Glu Gly			
171	615	630	635	640
172	ATA ATG GGA GCC AGG CTG GGG AAG CTG GCC CAG GCG CTC CAC CAG TGT			1968
173	Ile Lys Gly Ala Thr Val Gly Lys Leu Ala Gln Ala Leu His Gln Cys			
174	645	650	655	
175	TCC AGG ATC GAC CTT CTG AGC AGC TTG ATT TAC GTC AGC CAG AAC			2013
176	Ser Arg Ile Asp Ser Leu Ser Ser Leu Ile Tyr Val Ser Gln Asn			
177	660	665	670	
178	TAA			2016
179	(i) INFORMATION FOR SEQ ID NO: 2:			
180	(i) SEQUENCE CHARACTERISTICS:			
181	(A) LENGTH: 671 amino acids			
182	(B) TYPE: amino acid			
183	(C) TOPOLOGY: linear			
184	(D) MOLECULE TYPE: protein			
185	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:			
186	Met Gln Pro Asp Met Ser Leu Asn Val Ile Lys Met Lys Ser Ser Asp			
187	1	5	10	15
188	Phe Leu Glu Ser Ala Glu Leu Asp Ser Gly Gly Phe Glu Lys Val Ser			
189	20	25	30	
190	Leu Cys Phe His Arg Thr Gln Gly Leu Met Ile Met Lys Thr Val Tyr			
191	35	40	45	
192	Lys Gly Pro Asn Cys Ile Glu His Asn Glu Ala Leu Glu Glu Ala			
193	50	55	60	
194	Lys Met Met Asn Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly			
195	65	70	75	80
196	Val Ile Ile Glu Glu Gly Lys Tyr Ser Leu Val Met Glu Tyr Met Glu			
197	85	90	95	
198	Lys Gly Asn Leu Met His Val Leu Lys Ala Glu Met Ser Thr Pro Leu			

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200 100 105 110
201 Ser Val Lys Gly Arg Ile Ile Leu Glu Ile Ile Ile Gly Met Cys Thr
202 115 120 125
203 Leu His Gly Lys Gly Val Ile Ile Ile Lys Asp Leu Lys Pro Glu Asn Ile
204 130 135 140
205 Leu Val Asp Asn Asp Ile Ile Ile Lys Ile Ala Asp Leu Gly Leu Ala
206 145 150 155 160
207 Ser Phe Lys Met Trp Ser Lys Leu Asn Asn Glu Glu His Asn Glu Leu
208 165 170 175
209 Arg Glu Val Asp Gly Thr Ala Lys Lys Asn Gly Gly Thr Leu Tyr Tyr
210 180 185 190
211 Met Ala Pro Glu His Leu Asn Asp Val Asn Ala Lys Pro Thr Glu Lys
212 195 200 205
213 Ser Asp Val Tyr Ser Phe Ala Val Val Leu Trp Ala Ile Phe Ala Asn
214 210 215 220
215 Lys Glu Pro Tyr Glu Asn Ala Ile Cys Glu Gln Gln Leu Ile Met Cys
216 225 230 235 240
217 Ile Lys Ser Gly Asn Arg Pro Asp Val Asp Asp Ile Thr Glu Tyr Cys
218 245 250 255
219 Pro Arg Glu Ile Ile Ser Leu Met Lys Leu Cys Trp Glu Ala Asn Pro
220 260 265 270
221 Glu Ala Arg Pro Thr Phe Pro Gly Ile Glu Glu Lys Phe Arg Pro Phe
222 275 280 285
223 Tyr Leu Ser Gln Leu Glu Glu Ser Val Glu Glu Asp Val Lys Ser Leu
224 290 295 300
225 Lys Lys Glu Tyr Ser Asn Asn Glu Asn Ala Val Val Lys Arg Met Gln Ser
226 305 310 315 320
227 Leu Gln Leu Asp Cys Val Ala Val Pro Ser Ser Arg Ser Asn Ser Ala
228 325 330 335
229 Thr Glu Gln Pro Gly Ser Leu His Ser Ser Gln Gly Leu Gly Met Gly
230 340 345 350
231 Pro Val Glu Gln Ser Trp Phe Ala Pro Ser Leu Gln His Pro Gln Gln
232 355 360 365
233 Glu Asn Glu Pro Ser Leu Gln Ser Lys Leu Gln Asp Glu Ala Asn Tyr
234 370 375 380
235 His Leu Tyr Gly Ser Arg Met Asp Arg Gln Thr Lys Gln Gln Pro Arg
236 385 390 395 400
237 Gln Asn Val Ala Tyr Asn Arg Glu Glu Glu Arg Arg Arg Arg Val Ser
238 405 410 415
239 His Asp Pro Phe Ala Gln Gln Arg Pro Tyr Glu Asn Phe Gln Asn Thr
240 420 425 430
241 Glu Gly Lys Gly Thr Val Tyr Ser Ser Ala Ala Ser His Gly Asn Ala
242 435 440 445
243 Val His Gln Pro Ser Gly Leu Thr Ser Gln Pro Gln Val Leu Tyr Gln
244 450 455 460
245 Asn Asn Gly Leu Tyr Ser Ser His Gly Phe Gly Thr Arg Pro Leu Asp
246 465 470 475 480
247 Pro Gly Thr Ala Gly Pro Arg Val Trp Tyr Arg Pro Ile Pro Ser His
248 485 490 495

VERIFICATION SUMMARY

PATENT APPLICATION: **US/09/758,003**

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Input Set : **N:\Crf3\RULE60\09758003.txt**

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L:24 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:25 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]